



IFW16

RAW SEQUENCE LISTING

DATE: 08/27/2004

PATENT APPLICATION: US/10/798,923A

TIME: 11:17:34

Input Set : A:\ISIS0124-100 (RTS0739) SEQ(rev).txt

Output Set: N:\CRF4\08272004\J798923A.raw

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3 <110> APPLICANT: Kenneth W. Dobie
4     Susan M. Freier
6 <120> TITLE OF INVENTION: MODULATION OF ACE2 EXPRESSION
8 <130> FILE REFERENCE: RTS-0739US
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/798,923A
C--> 10 <141> CURRENT FILING DATE: 2004-03-10
10 <160> NUMBER OF SEQ ID NOS: 152
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 20
15 <212> TYPE: DNA
16 <213> ORGANISM: Artificial Sequence
18 <220> FEATURE:
20 <223> OTHER INFORMATION: Antisense compound
22 <400> SEQUENCE: 1
23 tccgtcatcg ctctcaggg
26 <210> SEQ ID NO: 2
27 <211> LENGTH: 20
28 <212> TYPE: DNA
29 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
33 <223> OTHER INFORMATION: Antisense compound
35 <400> SEQUENCE: 2
36 gtgcgcgcga gcccgaaatc
39 <210> SEQ ID NO: 3
40 <211> LENGTH: 20
41 <212> TYPE: DNA
42 <213> ORGANISM: Artificial Sequence
44 <220> FEATURE:
46 <223> OTHER INFORMATION: Antisense compound
48 <400> SEQUENCE: 3
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52 <210> SEQ ID NO: 4
53 <211> LENGTH: 3405
54 <212> TYPE: DNA
55 <213> ORGANISM: H. sapiens
57 <220> FEATURE:
59 <220> FEATURE:
60 <221> NAME/KEY: CDS
61 <222> LOCATION: (104)...(2521)
63 <400> SEQUENCE: 4
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66 gggaaagtca ttcagtgat gtgatcttgg ctacagggg acg atg tca agc tct 115
67                                     Met Ser Ser Ser

```



20

20

20

60

115

Met Ser Ser Ser

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68                                     1
70 tcc tgg ctc ctt ctc agc ctt gtt gct gta act gct gct cag tcc acc      163
71 Ser Trp Leu Leu Leu Ser Leu Val Ala Val Thr Ala Ala Gln Ser Thr
72   5                               10                               15                               20
74 att gag gaa cag gcc aag aca ttt ttg gac aag ttt aac cac gaa gcc      211
75 Ile Glu Glu Gln Ala Lys Thr Phe Leu Asp Lys Phe Asn His Glu Ala
76                               25                               30                               35
78 gaa gac ctg ttc tat caa agt tca ctt gct tct tgg aat tat aac acc      259
79 Glu Asp Leu Phe Tyr Gln Ser Ser Leu Ala Ser Trp Asn Tyr Asn Thr
80                               40                               45                               50
82 aat att act gaa gag aat gtc caa aac atg aat aat gct ggg gac aaa      307
83 Asn Ile Thr Glu Glu Asn Val Gln Asn Met Asn Asn Ala Gly Asp Lys
84                               55                               60                               65
86 tgg tct gcc ttt tta aag gaa cag tcc aca ctt gcc caa atg tat cca      355
87 Trp Ser Ala Phe Leu Lys Glu Gln Ser Thr Leu Ala Gln Met Tyr Pro
88   70                               75                               80
90 cta caa gaa att cag aat ctc aca gtc aag ctt cag ctg cag gct ctt      403
91 Leu Gln Glu Ile Gln Asn Leu Thr Val Lys Leu Gln Leu Gln Ala Leu
92  85                               90                               95                               100
94 cag caa aat ggg tct tca gtg ctc tca gaa gac aag agc aaa cgg ttg      451
95 Gln Gln Asn Gly Ser Ser Val Leu Ser Glu Asp Lys Ser Lys Arg Leu
96                               105                               110                               115
98 aac aca att cta aat aca atg agc acc atc tac agt act gga aaa gtt      499
99 Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser Thr Gly Lys Val
100                               120                               125                               130
102 tgt aac cca gat aat cca caa gaa tgc tta tta ctt gaa cca ggt ttg      547
103 Cys Asn Pro Asp Asn Pro Gln Glu Cys Leu Leu Leu Glu Pro Gly Leu
104                               135                               140                               145
106 aat gaa ata atg gca aac agt tta gac tac aat gag agg ctc tgg gct      595
107 Asn Glu Ile Met Ala Asn Ser Leu Asp Tyr Asn Glu Arg Leu Trp Ala
108                               150                               155                               160
110 tgg gaa agc tgg aga tct gag gtc ggc aag cag ctg agg cca tta tat      643
111 Trp Glu Ser Trp Arg Ser Glu Val Gly Lys Gln Leu Arg Pro Leu Tyr
112 165                               170                               175                               180
114 gaa gag tat gtg gtc ttg aaa aat gag atg gca aga gca aat cat tat      691
115 Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg Ala Asn His Tyr
116                               185                               190                               195
118 gag gac tat ggg gat tat tgg aga gga gac tat gaa gta aat ggg gta      739
119 Glu Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu Val Asn Gly Val
120                               200                               205                               210
122 gat ggc tat gac tac agc cgc ggc cag ttg att gaa gat gtg gaa cat      787
123 Asp Gly Tyr Asp Tyr Ser Arg Gly Gln Leu Ile Glu Asp Val Glu His
124                               215                               220                               225
126 acc ttt gaa gag att aaa cca tta tat gaa cat ctt cat gcc tat gtg      835
127 Thr Phe Glu Glu Ile Lys Pro Leu Tyr Glu His Leu His Ala Tyr Val
128                               230                               235                               240
130 agg gca aag ttg atg aat gcc tat cct tcc tat atc agt cca att gga      883
131 Arg Ala Lys Leu Met Asn Ala Tyr Pro Ser Tyr Ile Ser Pro Ile Gly
132 245                               250                               255                               260

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134	tgc	ctc	cct	gct	cat	ttg	ctt	ggt	gat	atg	tgg	ggt	aga	ttt	tgg	aca	931
135	Cys	Leu	Pro	Ala	His	Leu	Leu	Gly	Asp	Met	Trp	Gly	Arg	Phe	Trp	Thr	
136					265					270					275		
138	aat	ctg	tac	tct	ttg	aca	gtt	ccc	ttt	gga	cag	aaa	cca	aac	ata	gat	979
139	Asn	Leu	Tyr	Ser	Leu	Thr	Val	Pro	Phe	Gly	Gln	Lys	Pro	Asn	Ile	Asp	
140				280					285					290			
142	gtt	act	gat	gca	atg	gtg	gac	cag	gcc	tgg	gat	gca	cag	aga	ata	ttc	1027
143	Val	Thr	Asp	Ala	Met	Val	Asp	Gln	Ala	Trp	Asp	Ala	Gln	Arg	Ile	Phe	
144			295					300					305				
146	aag	gag	gcc	gag	aag	ttc	ttt	gta	tct	gtt	ggt	ctt	cct	aat	atg	act	1075
147	Lys	Glu	Ala	Glu	Lys	Phe	Phe	Val	Ser	Val	Gly	Leu	Pro	Asn	Met	Thr	
148		310					315					320					
150	caa	gga	ttc	tgg	gaa	aat	tcc	atg	cta	acg	gac	cca	gga	aat	gtt	cag	1123
151	Gln	Gly	Phe	Trp	Glu	Asn	Ser	Met	Leu	Thr	Asp	Pro	Gly	Asn	Val	Gln	
152	325				330					335					340		
154	aaa	gca	gtc	tgc	cat	ccc	aca	gct	tgg	gac	ctg	ggg	aag	ggc	gac	ttc	1171
155	Lys	Ala	Val	Cys	His	Pro	Thr	Ala	Trp	Asp	Leu	Gly	Lys	Gly	Asp	Phe	
156				345					350					355			
158	agg	atc	ctt	atg	tgc	aca	aag	gtg	aca	atg	gac	gac	ttc	ctg	aca	gct	1219
159	Arg	Ile	Leu	Met	Cys	Thr	Lys	Val	Thr	Met	Asp	Asp	Phe	Leu	Thr	Ala	
160			360					365					370				
162	cat	cat	gag	atg	ggg	cat	atc	cag	tat	gat	atg	gca	tat	gct	gca	caa	1267
163	His	His	Glu	Met	Gly	His	Ile	Gln	Tyr	Asp	Met	Ala	Tyr	Ala	Ala	Gln	
164			375				380					385					
166	cct	ttt	ctg	cta	aga	aat	gga	gct	aat	gaa	gga	ttc	cat	gaa	gct	gtt	1315
167	Pro	Phe	Leu	Leu	Arg	Asn	Gly	Ala	Asn	Glu	Gly	Phe	His	Glu	Ala	Val	
168		390				395						400					
170	ggg	gaa	atc	atg	tca	ctt	tct	gca	gcc	aca	cct	aag	cat	tta	aaa	tcc	1363
171	Gly	Glu	Ile	Met	Ser	Leu	Ser	Ala	Ala	Thr	Pro	Lys	His	Leu	Lys	Ser	
172	405				410					415				420			
174	att	ggt	ctt	ctg	tca	ccc	gat	ttt	caa	gaa	gac	aat	gaa	aca	gaa	ata	1411
175	Ile	Gly	Leu	Leu	Ser	Pro	Asp	Phe	Gln	Glu	Asp	Asn	Glu	Thr	Glu	Ile	
176				425					430					435			
178	aac	ttc	ctg	ctc	aaa	caa	gca	ctc	acg	att	gtt	ggg	act	ctg	cca	ttt	1459
179	Asn	Phe	Leu	Leu	Lys	Gln	Ala	Leu	Thr	Ile	Val	Gly	Thr	Leu	Pro	Phe	
180			440					445					450				
182	act	tac	atg	tta	gag	aag	tgg	agg	tgg	atg	gtc	ttt	aaa	ggg	gaa	att	1507
183	Thr	Tyr	Met	Leu	Glu	Lys	Trp	Arg	Trp	Met	Val	Phe	Lys	Gly	Glu	Ile	
184			455				460					465					
186	ccc	aaa	gac	cag	tgg	atg	aaa	aag	tgg	tgg	gag	atg	aag	cga	gag	ata	1555
187	Pro	Lys	Asp	Gln	Trp	Met	Lys	Lys	Trp	Trp	Glu	Met	Lys	Arg	Glu	Ile	
188		470				475					480						
190	gtt	ggg	gtg	gtg	gaa	cct	gtg	ccc	cat	gat	gaa	aca	tac	tgt	gac	ccc	1603
191	Val	Gly	Val	Val	Glu	Pro	Val	Pro	His	Asp	Glu	Thr	Tyr	Cys	Asp	Pro	
192	485				490					495				500			
194	gca	tct	ctg	ttc	cat	gtt	tct	aat	gat	tac	tca	ttc	att	cga	tat	tac	1651
195	Ala	Ser	Leu	Phe	His	Val	Ser	Asn	Asp	Tyr	Ser	Phe	Ile	Arg	Tyr	Tyr	
196				505					510				515				
198	aca	agg	acc	ctt	tac	caa	ttc	cag	ttt	caa	gaa	gca	ctt	tgt	caa	gca	1699

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199	Thr	Arg	Thr	Leu	Tyr	Gln	Phe	Gln	Phe	Gln	Glu	Ala	Leu	Cys	Gln	Ala	
200				520				525					530				
202	gct	aaa	cat	gaa	ggc	cct	ctg	cac	aaa	tgt	gac	atc	tca	aac	tct	aca	1747
203	Ala	Lys	His	Glu	Gly	Pro	Leu	His	Lys	Cys	Asp	Ile	Ser	Asn	Ser	Thr	
204			535					540					545				
206	gaa	gct	gga	cag	aaa	ctg	ttc	aat	atg	ctg	agg	ctt	gga	aaa	tca	gaa	1795
207	Glu	Ala	Gly	Gln	Lys	Leu	Phe	Asn	Met	Leu	Arg	Leu	Gly	Lys	Ser	Glu	
208		550					555					560					
210	ccc	tgg	acc	cta	gca	ttg	gaa	aat	gtt	gta	gga	gca	aag	aac	atg	aat	1843
211	Pro	Trp	Thr	Leu	Ala	Leu	Glu	Asn	Val	Val	Gly	Ala	Lys	Asn	Met	Asn	
212	565					570					575					580	
214	gta	agg	cca	ctg	ctc	aac	tac	ttt	gag	ccc	tta	ttt	acc	tgg	ctg	aaa	1891
215	Val	Arg	Pro	Leu	Leu	Asn	Tyr	Phe	Glu	Pro	Leu	Phe	Thr	Trp	Leu	Lys	
216				585						590					595		
218	gac	cag	aac	aag	aat	tct	ttt	gtg	gga	tgg	agt	acc	gac	tgg	agt	cca	1939
219	Asp	Gln	Asn	Lys	Asn	Ser	Phe	Val	Gly	Trp	Ser	Thr	Asp	Trp	Ser	Pro	
220			600						605				610				
222	tat	gca	gac	caa	agc	atc	aaa	gtg	agg	ata	agc	cta	aaa	tca	gct	ctt	1987
223	Tyr	Ala	Asp	Gln	Ser	Ile	Lys	Val	Arg	Ile	Ser	Leu	Lys	Ser	Ala	Leu	
224			615					620					625				
226	gga	gat	aaa	gca	tat	gaa	tgg	aac	gac	aat	gaa	atg	tac	ctg	ttc	cga	2035
227	Gly	Asp	Lys	Ala	Tyr	Glu	Trp	Asn	Asp	Asn	Glu	Met	Tyr	Leu	Phe	Arg	
228		630				635					640						
230	tca	tct	gtt	gca	tat	gct	atg	agg	cag	tac	ttt	tta	aaa	gta	aaa	aat	2083
231	Ser	Ser	Val	Ala	Tyr	Ala	Met	Arg	Gln	Tyr	Phe	Leu	Lys	Val	Lys	Asn	
232	645					650					655					660	
234	cag	atg	att	ctt	ttt	ggg	gag	gag	gat	gtg	cga	gtg	gct	aat	ttg	aaa	2131
235	Gln	Met	Ile	Leu	Phe	Gly	Glu	Glu	Asp	Val	Arg	Val	Ala	Asn	Leu	Lys	
236				665						670					675		
238	cca	aga	atc	tcc	ttt	aat	ttc	ttt	gtc	act	gca	cct	aaa	aat	gtg	tct	2179
239	Pro	Arg	Ile	Ser	Phe	Asn	Phe	Phe	Val	Thr	Ala	Pro	Lys	Asn	Val	Ser	
240			680						685				690				
242	gat	atc	att	cct	aga	act	gaa	gtt	gaa	aag	gcc	atc	agg	atg	tcc	cgg	2227
243	Asp	Ile	Ile	Pro	Arg	Thr	Glu	Val	Glu	Lys	Ala	Ile	Arg	Met	Ser	Arg	
244			695					700					705				
246	agc	cgt	atc	aat	gat	gct	ttc	cgt	ctg	aat	gac	aac	agc	cta	gag	ttt	2275
247	Ser	Arg	Ile	Asn	Asp	Ala	Phe	Arg	Leu	Asn	Asp	Asn	Ser	Leu	Glu	Phe	
248		710				715					720						
250	ctg	ggg	ata	cag	cca	aca	ctt	gga	cct	cct	aac	cag	ccc	cct	gtt	tcc	2323
251	Leu	Gly	Ile	Gln	Pro	Thr	Leu	Gly	Pro	Pro	Asn	Gln	Pro	Pro	Val	Ser	
252	725					730					735					740	
254	ata	tgg	ctg	att	gtt	ttt	gga	gtt	gtg	atg	gga	gtg	ata	gtg	gtt	ggc	2371
255	Ile	Trp	Leu	Ile	Val	Phe	Gly	Val	Val	Met	Gly	Val	Ile	Val	Val	Gly	
256				745						750					755		
258	att	gtc	atc	ctg	atc	ttc	act	ggg	atc	aga	gat	cgg	aag	aag	aaa	aat	2419
259	Ile	Val	Ile	Leu	Ile	Phe	Thr	Gly	Ile	Arg	Asp	Arg	Lys	Lys	Lys	Asn	
260			760						765				770				
262	aaa	gca	aga	agt	gga	gaa	aat	cct	tat	gcc	tcc	atc	gat	att	agc	aaa	2467
263	Lys	Ala	Arg	Ser	Gly	Glu	Asn	Pro	Tyr	Ala	Ser	Ile	Asp	Ile	Ser	Lys	

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264          775          780          785
266 gga gaa aat aat cca gga ttc caa aac act gat gat gtt cag acc tcc 2515
267 Gly Glu Asn Asn Pro Gly Phe Gln Asn Thr Asp Val Gln Thr Ser
268          790          795          800
270 ttt tag aaaaatctat gtttttcctc ttgaggtgat tttgttgat gtaaagtta 2571
271 Phe
272 805
274 atttcatggt atagaaaata taagatgata aagatatcat taaatgtcaa aactatgact 2631
276 ctgttcagaa aaaaaattgt ccaaagacaa catggccaag gagagagcat cttcattgac 2691
278 attgctttca gtatttattt ctgtctctgg atttgacttc tgttctgttt ctttaataagg 2751
280 attttgtatt agagtatatt agggaaagtg tgtatttggt ctcacaggct gttcagggat 2811
282 aatctaaatg taaatgtctg ttgaatttct gaagttgaaa acaaggatat atcattggag 2871
284 caagtgttg atcttgtatg gaatatggat ggatcacttg taaggacagt gcctgggaac 2931
286 tgggtgtagct gcaaggattg agaatggcat gcattagctc actttcattt aatccattgt 2991
288 caaggatgac atgcttttctt cacagtaact cagttcaagt actatggtga tttgcctaca 3051
290 gtgatgtttg gaatcgatca tgcttttctt aaggtgacag gtctaaagag agaagaatcc 3111
292 agggaacagg tagaggacat tgcttttttca cttccaagggt gcttgatcaa catctccctg 3171
294 acaacacaaa actagagcca ggggcctcgg tgaactccca gagcatgcct gatagaaact 3231
296 catttctact gttctctaac tgtggagtga atggaaattc caactgtatg ttcaccctct 3291
298 gaagtgggta cccagctctt taaatctttt gtatttgctc acagtgtttg agcagtgctg 3351
300 agcacaagc agacactcaa taaatgctag atttacacac tcaaaaaaaaa aaaa 3405
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304 <211> LENGTH: 21
305 <212> TYPE: DNA
306 <213> ORGANISM: Artificial Sequence
308 <220> FEATURE:
310 <223> OTHER INFORMATION: PCR Primer
312 <400> SEQUENCE: 5
313 ggctccttct cagccttggt g 21
316 <210> SEQ ID NO: 6
317 <211> LENGTH: 23
318 <212> TYPE: DNA
319 <213> ORGANISM: Artificial Sequence
321 <220> FEATURE:
323 <223> OTHER INFORMATION: PCR Primer
325 <400> SEQUENCE: 6
326 gcttcgtggt taaacttgctc caa 23
329 <210> SEQ ID NO: 7
330 <211> LENGTH: 29
331 <212> TYPE: DNA
332 <213> ORGANISM: Artificial Sequence
334 <220> FEATURE:
336 <223> OTHER INFORMATION: PCR Probe
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339 tgtaactgct gctcagtcca ccattgagg 29
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343 <211> LENGTH: 19
344 <212> TYPE: DNA
345 <213> ORGANISM: Artificial Sequence

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VERIFICATION SUMMARY

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:10 M:270 C: Current Application Number differs, Replaced Current Application No
:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date